BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program [blastp ⬍] Matrix [BLOSUM62 ⬍]

Parameters used in BLASTN program only:
Reward for a match: [   ] **Penalty for a mismatch:** [   ]
☐ Use Mega BLAST   Strand option [Not Applicable ⬍]

Open gap [11] and extension gap [1] penalties
gap x_dropoff [50] expect [10] word size [3] Filter ☑

Sequence 1 Enter accession or GI [b To P] or download from file [   ]

or sequence in FASTA format from: [   ] to: [   ]

```
gyvvtnnnvvanatvikvqisagrkraakmvgkaprsalailqiqnpknitalkmaasaai
rvgdytvaignpfglgetvtsgivsalgrsglnaenyenfiqtdaainrgnsggalvnlng
eligintailapdggnigigfaipsnmvknltsqmveygqvkrgelgimgtelnselakam
kvdaqrgafvsqvlpnssaakagikagdvitslngkpissfaalraqvgtmpvgskltlgl
lrdgkqvnvnlelqqssqnqvdsssifngiegaemsnkgkdqgvvvnnvktgtpaaqiglk
kgdviiganqqavkniaelrkvldskpsvlalniqrgdstiyllmq
```

DEG P of E. coli

Sequence 2 Enter accession or GI [Gilbert] or download from file [   ]

or sequence in FASTA format from: [   ] to: [   ]

```
mglkkacltvlclivfcfgifytfdrvnhgernavsllkdklfneegepvnlifcytilqm
kvaerimaqhpgerfyvvlmsenrnekydyyfkqikdkaerayffhlpyglnksfnfiptm
aelkvksmllpkvkriylaslekvsiaaflstypdaeiktfddgtgnliqsssylgdefsv
ngtikrnfarmmigdwsiaktrnasdehytifkglknimddgrrkmtylplfdaselkagd
etggtvrillgspdkemkeisekaaknfniqyvaphprqtyglsgvttlnspyviedyilr
eikknphtryeiytffsgaaltmkdf
```

Gilbert
 # SEQ ID NO: 2

[Align] [Clear Input]

Comments and suggestions to: blast-help@ncbi.nlm.nih.gov
Credits to: Tatiana Tatusov *and* Tom Madden

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix BLOSUM62 ⬍ gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☑ Align

Sequence 1 lcl|seq_1 **Length** 473

Sequence 2 lcl|seq_2 **Length** 331

No significant similarity was found